



-37-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Caput, Daniel
Ferrara, Pascual
Laurent, Patrick
Vita, Natalio
- (ii) TITLE OF INVENTION: IL-13 receptor
- (iii) NUMBER OF SEQUENCES: 4
- (iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: renal
(H) CELL LINE: caki-1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGTGCCTGTC GCGGGGAGA GAGGCAATA CAAGGTTTAA AATCTCGGAG AAATGGCTTA 60
ATTCGTTTGC TTGGCTATCG GATGCTTATA TACCTTTCTG ATAAGCACAA CATTGGCTG 120
TACAAGCTTT TGCATTTCAT CTTGAGACAC CGAGATAAAA GTTAACCCTC CTCAGGATTT 180
TGAGATAGTG GATTATGAAG AGAACCCGGA TACTTAGGTT ATCTCTATTT GCAATGGCAA 240
CCCCCACTGT CTCTGGATCA TTTTGTGTTG TGAAGGAAT GCACAGTGGA ATATGAACTA 300
AAATACCGAA ACATTGGTAG TGAAACATGG AAGGCTAGTG TAGAGGTTAC CATCATTACT 360
AAGAATCTAC ATTACAAAGA TGGGTTTGAT CTTAACAAGG GCATTGAATT ATAGAAGGGC 420
GAAGATACAC ACGCTTTTAC CATGGCAATG CACAAATGGA TCAGAAGTTC AAAGTTCCAA 480
TTGCTAGGAG TGGGCAGAAA CTAATTATTG GATATCACCA CAAGGAATTC CAGAACTAA 540
AGTTCAGGAT TAAGTTTTGG GTAGAATGGA TTGCGTATAT TACAATTGGC AATATTTACT 600
CTGTTCTTGG AAACCTGGCA TAGGTTACAT TATGTCTGGG TACTTCTTGA TACCAATTAC 660
AACTTGTTTT ACTGGTATGA GGGCTTGGAT CATGCATTAA ATATATTTGG AAACAGTGTG 720

TTGATTACAT CAAGGCTGAT GGACAAAATA TAGGATGCAG ATTTCCCTAT TTGGCAATAA 780
 AGGAGCAGTG AGGCATCAGA CTATAAAGAT TTCTATATTT GTGTTAATGG ATCATCAGAG 840
 AACAAAGCCTG AAATATCAAG GAATCAGATC CAGTTATTTT ACTTTTCAGC TTCAAAATAT 900
 AGTTAAACCT TTGCCGCCAG TCAGTTGGAA ATATCTTACT TTTACTCGGG AGAGTTCATG 960
 TGAAATTAAG CTGAAATGGA GCATACCTTT GTTTAGGCGT GGACCTATTC CAGCAAGGTG 1020
 TTTTGATTAT GAAATTGAGA TCAGAGAAGA TGATACTACC GAAAGCATGG AGGAATTTTG 1080
 GTGACTGCTA CAGTTGAAAA TGAAACATAC ACCTTGAAAA CAACAAATGA AACCCGAATA 1140
 ATAGAGTTTT TAGTAGCAAT TATGCTTTGT AGTAAGAAGC AAAGTGAATA TTTATTGCTC 1200
 AGATGACGGA ATTTGGGCAA AGAATCAAGT AGTGAGTGGA GTGATAAACA ATGCTGGGAA 1260
 GGTGAAGACC TATCGAAGAA AACTTTGCTA GTAGCTGGGA TCGTTTCTGG CTACCATTTG 1320
 GTTTCATCTT AATATTAGTT ATATTTGTAA CCGGTCTGCT TAGTGAATGT TGC GTAAGCC 1380
 AAACACCTAC CCAAAAATGA TTCCAGAATT TTTCTGTGAT ACATGAAGAA GATTTGCATC 1440
 TTTCCATATC AAGAGACATG GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA 1500
 TATGAGTCTC AATAAACTGA ATTTTCTTG CGAATGTTG 1539

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Carcinoma
- (G) CELL TYPE: renal
- (H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Phe	Val	Cys	Leu	Ala	Ile	Gly	Cys	Leu	Tyr	Thr	Phe	Leu	Ile
1				5				10						15	
Ser	Thr	Thr	Phe	Gly	Cys	Thr	Ser	Ser	Ser	Asp	Thr	Glu	Ile	Lys	Val
			20				25						30		
Asn	Pro	Pro	Gln	Asp	Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr
		35					40					45			
Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser	Leu	Asp	His	Phe	Lys	Glu
	50					55					60				
Cys	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Gly	Ser	Glu	Thr
65					70					75				80	
Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His	Tyr	Lys	Asp	Gly	Phe	Asp

85										90					95				
Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His	Thr	Leu	Leu	Pro	Trp	Gln				
			100					105					110						
Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser	Trp	Ala	Glu	Thr	Thr	Tyr				
		115					120					125							
Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr	Lys	Val	Gln	Asp	Met	Asp				
	130					135					140								
Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu	Cys	Ser	Trp	Lys	Pro	Gly				
145					150					155					160				
Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn	Leu	Phe	Tyr	Trp	Tyr	Glu				
				165					170						175				
Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp	Tyr	Ile	Lys	Ala	Asp	Gly				
			180					185					190						
Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ala	Ser	Asp	Tyr	Lys				
		195					200					205							
Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser	Glu	Asn	Lys	Pro	Ile	Arg				
	210					215					220								
Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Leu	Pro				
225					230					235					240				
Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser	Ser	Cys	Glu	Ile	Lys	Leu				
				245					250					255					
Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro	Ala	Arg	Cys	Phe	Asp	Tyr				
			260					265					270						
Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr	Leu	Val	Thr	Ala	Thr	Val				
		275					280					285							
Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr	Asn	Glu	Thr	Arg	Gln	Leu				
	290					295					300								
Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly				
305					310					315					320				
Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys	Trp	Glu	Gly	Glu	Asp	Leu				
				325					330					335					
Ser	Lys	Lys	Thr	Leu	Leu	Arg	Phe	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu				
			340					345					350						
Ile	Leu	Val	Ile	Phe	Val	Thr	Gly	Leu	Leu	Leu	Arg	Lys	Pro	Asn	Thr				
		355					360					365							
Tyr	Pro	Lys	Met	Ile	Pro	Glu	Phe	Phe	Cys	Asp	Thr								
	370					375					380								

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4009 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
(F) TISSUE TYPE: Carcinoma
(G) CELL TYPE: RENAL
(H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAGCCCGGC CGGGCTCCGA GCGGAGAGGC TGCATGGAGT GGCCGGCGCG GCTCTGCGGG 60
CTGTGGGCGC TGCTGCTCTG CGCCGGCGGC GGGGGCGGGG GCGGGGGCGC CGCGCCTACG 120
GAAACTCAGC CACCTGTGAC AAATTTGAGT GTCTCTGTTG AAAACCTCTG CACAGTAATA 180
TGGACATGGA ATCCACCCGA GGGAGCCAGC TCAAATTGTA GTCTATGGTA TTTTAGTCAT 240
TTTGGCGACA AACAAGATAA GAAAATAGCT CCGGAAACTC GTCGTTCAAT AGAAGTACCC 300
CTGAATGAGA GGATTTGTCT GCAAGTGGGG TCCAGTGTA GCACCAATGA GAGTGAGAAG 360
CCTAGCATTT TGGTTGAAAA ATGCATCTCA CCCCAGAAG GTGATCCTGA GTCTGCTGTG 420
ACTGAGCTTC AATGCATTTG GCACAACCTG AGCTACATGA AGTGTTCCTG GCTCCCTGGA 480
AGGAATACCA GTCCCGACAC TAACTATACT CTCTACTATT GGCACAGAAG CCTGGAAAAA 540
ATTCATCAAT GTGAAAACAT CTTTAGAGAA GGCCAATACT TTGGTTGTTT CTTTGATCTG 600
ACCAAAGTGA AGGATTCCAG TTTGAACAA CACAGTGTCC AAATAATGGT CAAGGATAAT 660
GCAGGAAAAA TTAAACCATC CTTCAATATA GTGCCTTTAA CTTCCCGTGT GAAACCTGAT 720
CCTCCACATA TTAAAAACCT CTCCTTCCAC AATGATGACC TATATGTGCA ATGGGAGAAT 780
CCACAGAATT TTATTAGCAG ATGCCTATTT TATGAAGTAG AAGTCAATAA CAGCCAACT 840
GAGACACATA ATGTTTTCTA CGTCCAAGAG GCTAAATGTG AGAATCCAGA ATTTGAGAGA 900
AATGTGGAGA ATACATCTTG TTTCATGGTC CCTGGTGTTT TTCCTGATAC TTTGAACACA 960
GTCAGAATAA GAGTCAAAAC AAATAAGTTA TGCTATGAGG ATGACAACT CTGGAGTAAT 1020
TGGAGCCAAG AAATGAGTAT AGGTAAGAAG CGCAATTCCA CACTCTACAT AACCATGTTA 1080
CTCATTGTTT CAGTCATCGT CGCAGGTGCA ATCATAGTAC TCCTGCTTTA CCTAAAAAGG 1140
CTCAAGATTA TTATATCCC TCCAATTCCT GATCCTGGCA AGATTTTAA AGAAATGTTT 1200
GGAGACCAGA ATGATGATAC TCTGCACTGG AAGAAGTACG ACATCTATGA GAAGCAAACC 1260
AAGGAGGAAA CCGACTCTGT AGTGCTGATA GAAACCTGA AGAAAGCCTC TCAGTGATGG 1320

AGATAATTTA TTTTACCTT CACTGTGACC TTGAGAAGAT TCTTCCCATT CTCCATTTGT 1380
TATCTGGGAA CTTATTAAAT GGAACTGAA ACTACTGCAC CATTTAAAAA CAGGCAGCTC 1440
ATAAGAGCCA CAGGTCTTTA TGTGAGTCG CGCACCGAAA AACTAAAAAT AATGGGCGCT 1500
TTGGAGAAGA GTGTGGAGTC ATTCTCATTG AATTATAAAA GCCAGCAGGC TTCAAAC TAG 1560
GGGACAAAGC AAAAAGTGAT GATAGTGGTG GAGTTAATCT TATCAAGAGT TGTGACAACT 1620
TCCTGAGGGA TCTATACTTG CTTTGTGTTT TTTGTGTCAA CATGAACAAA TTTTATTTGT 1680
AGGGGAACTC ATTTGGGGTG CAAATGCTAA TGTCAAACCTT GAGTCACAAA GAACATGTAG 1740
AAAACAAAAT GGATAAAATC TGATATGTAT TGTTTGGGAT CCTATTGAAC CATGTTTGTG 1800
GCTATTAAAA CTCTTTTAAC AGTCTGGGCT GGGTCCGGTG GCTCACGCCT GTAATCCCAG 1860
CAATTTGGGA GTCCGAGGCG GCGGATCAC TCGAGGTCAG GAGTTCCAGA CCAGCCTGAC 1920
CAAAATGGTG AAACCTCCTC TCTACTAAAA CTACAAAAT TAACTGGGTG TGGTGGCGCG 1980
TGCCTGTAAT CCCAGCTACT CGGGAAGCTG AGGCAGGTGA ATTGTTTGAA CCTGGGAGGT 2040
GGAGGTTGCA GTGAGCAGAG ATCACACCAC TGCACTCTAG CCTGGGTGAC AGAGCAAGAC 2100
TCTGTCTAAA AAACAAAACA AAACAAAACA AAACAAAAAA ACCTCTTAAT ATTCTGGAGT 2160
CATCATTCCC TTCGACAGCA TTTTCCTCTG CTTTGAAAGC CCCAGAAATC AGTGTGGGCC 2220
ATGATGACAA CTACAGAAAA ACCAGAGGCA GCTTCTTTGC CAAGACCTTT CAAAGCCATT 2280
TTAGGCTGTT AGGGGCAGTG GAGGTAGAAT GACTCCTTGG GTATTAGAGT TTCAACCATG 2340
AAGTCTCTAA CAATGTATTT TCTTCACCTC TGCTACTCAA GTAGCATTTA CTGTGTCTTT 2400
GGTTTGTGCT AGGCCCCCGG GTGTGAAGCA CAGACCCTT CCAGGGGTTT ACAGTCTATT 2460
TGAGACTCCT CAGTTCTTGC CACTTTTTTT TTTAATCTCC ACCAGTCATT TTCAGACCT 2520
TTTAACTCCT CAATTCCAAC ACTGATTTCC CTTTTGTCAT TCTCCCTCCT TCCCTTCCTT 2580
GTAGCCTTTT GACTTTCATT GGAAATTAGG ATGTAAATCT GCTCAGGAGA CCTGGAGGAG 2640
CAGAGGATAA TTAGCATCTC AGGTAAAGTG TGAGTAATCT GAGAAACAAT GACTAATTCT 2700
TGCATATTTT GTAACCTCCA TGTGAGGGTT TTCAGATTG ATATTTGTGC ATTTTCTAAA 2760
CAGAGATGAG GTGGTATCTT CACGTAGAAC ATTGGTATTC GCTTGAGAAA AAAAGAATAG 2820
TTGAACCTAT TTCTCTTTCT TTACAAGATG GGTCCAGGAT TCCTCTTTT TCTGCCATAA 2880
ATGATTAATT AAATAGCTTT TGTGTCTTAC ATTGGTAGCC AGCCAGCCAA GGCTCTGTTT 2940
ATGCTTTTGG GGGGCATATA TTGGGTCCA TTCTCACCTA TCCACACAAC ATATCCGTAT 3000
ATATCCCCTC TACTCTTACT TCCCCAAAT TTAAAGAAGT ATGGGAAATG AGAGGCATTT 3060
CCCCACCCC ATTTCTCTCC TCACACACAG ACTCATATTA CTGGTAGGAA CTTGAGAACT 3120
TTATTTCCAA GTTGTTCAAA CATTTACCAA TCATATTAAT ACAATGATGC TATTTGCAAT 3180

TCCTGCTCCT AGGGGAGGGG AGATAAGAAA CCCTCACTCT CTACAGGTTT GGGTACAAGT 3240
 GGCAACCTGC TTCCATGGCC GTGTAGAAGC ATGGTGCCCT GGCTTCTCTG AGGAAGCTGG 3300
 GGTTTCATGAC AATGGCAGAT GTAAAGTTAT TCTTGAAGTC AGATTGAGGC TGGGAGACAG 3360
 CCGTAGTAGA TGTTCTACTT TGTTCTGCTG TTCTCTAGAA AGAATATTTG GTTTTCTGT 3420
 ATAGGAATGA GATTAATTCC TTTCCAGGTA TTTTATAATT CTGGGAAGCA AAACCCATGC 3480
 CTCCCCCTAG CCATTTTTTAC TGTTATCCTA TTTAGATGGC CATGAAGAGG ATGCTGTGAA 3540
 ATTCCCAACA AACATTGATG CTGACAGTCA TGCAGTCTGG GAGTGGGGAA GTGATCTTTT 3600
 GTTCCCATCC TCTTCTTTTA GCAGTAAAAT AGCTGAGGGA AAAGGGAGGG AAAAGGAAGT 3660
 TATGGGAATA CCTGTGGTGG TTGTGATCCC TAGGTCTTGG GAGCTCTTGG AGGTGTCTGT 3720
 ATCAGTGGAT TTCCCATCCC CTGTGGGAAA TTAGTAGGCT CATTACTGT TTTAGGTCTA 3780
 GCCTATGTGG ATTTTTTCTT AACATACCTA AGCAAACCCA GTGTCAGGAT GGTAATTCTT 3840
 ATTCTTTCGT TCAGTTAAGT TTTTCCCTTC ATCTGGGCAC TGAAGGGATA TGTGAAACAA 3900
 TGTTAACATT TTTGGTAGTC TTCAACCAGG GATTGTTTCT GTTTAACTTC TTATAGGAAA 3960
 GCTTGAGTAA AATAAATATT GTCTTTTGT ATGTCACCCA AAAAAAAAAA 4009

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Carcinoma
- (G) CELL TYPE: renal
- (H) CELL LINE: Caki-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Glu	Trp	Pro	Ala	Arg	Leu	Cys	Gly	Leu	Trp	Ala	Leu	Leu	Leu	Cys
1				5					10					15	
Ala	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Ala	Pro	Thr	Glu	Thr
			20						25					30	Gln
Pro	Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val
			35				40					45			
Ile	Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu
		50				55					60				
Trp	Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro
65					70					75					80
Glu	Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu
				85					90					95	

Gln Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile
 100 105 110
 Leu Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala
 115 120 125
 Val Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys
 130 135 140
 Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu
 145 150 155 160
 Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile
 165 170 175
 Phe Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val
 180 185 190
 Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp
 195 200 205
 Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser
 210 215 220
 Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn
 225 230 235 240
 Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg
 245 250 255
 Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His
 260 265 270
 Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu
 275 280 285
 Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro
 290 295 300
 Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys
 305 310 315 320
 Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile
 325 330 335
 Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val
 340 345 350
 Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys
 355 360 365
 Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile
 370 375 380
 Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys
 385 390 395 400
 Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val
 405 410 415
 Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425